STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/527,258_

Source: _PCT/10_

Date Processed by STIC: _3/22/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building. 401 Dulany Street. Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/527,258

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
        Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                          prevent "wrapping."

·2 _____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
        Numbering   use space characters, instead.

4 _____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                    ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length   Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                          each n or Xaa can only represent a single residue. Please present the maximum number of each
                          residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
        "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                      previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                      the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                      Artificial or Unknown sequences.

7 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
        (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                            (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                            (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                            This sequence is intentionally skipped

                            Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
        (NEW RULES)   <210> sequence id number
                            <400> sequence id number
                            000

9 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
        (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                              In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
         Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                         is Artificial Sequence

11 _____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                        Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                        "Unknown." Please explain source of genetic material in <220> to <223> section.
                        (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
         "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                        listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

RAW SEQUENCE LISTING   DATE: 03/22/2005
PATENT APPLICATION: US/10/527,258   TIME: 09:49:38

```
         Input Set : A:\PTO.SR.txt
         Output Set: N:\CRF4\03222005\J527258.raw

   3 <110> APPLICANT: KUREHA CHEMICAL INDUSTRY COMPANY, LIMITED
   4       YAMAMOTO, Mikio
   5       YAMAMOTO, Naoki
   7 <120> TITLE OF INVENTION: METHOD FOR PREPARATION OF EXPRESSED GENE IDENTIFICATION CDNA
TAG AND
   8       METHOD FOR ANALYSIS OF GENE EXPRESSION
  10 <130> FILE REFERENCE: 0701004WO1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/527,258
C--> 12 <141> CURRENT FILING DATE: 2005-03-09
  12 <160> NUMBER OF SEQ ID NOS: 65
  14 <170> SOFTWARE: PatentIn version 3.1
  16 <210> SEQ ID NO: 1
  17 <211> LENGTH: 21
  18 <212> TYPE: DNA
  19 <213> ORGANISM: Artificial Sequence
  21 <220> FEATURE:
  22 <223> OTHER INFORMATION: Artificail Sequence
  24 <220> FEATURE:
  25 <221> NAME/KEY: misc_feature
  26 <222> LOCATION: (1)..(7)
  27 <223> OTHER INFORMATION: n stands for any base
  30 <220> FEATURE:
  31 <221> NAME/KEY: misc_feature
  32 <222> LOCATION: (14)..(18)
  33 <223> OTHER INFORMATION: n stands for any base
  36 <400> SEQUENCE: 1
W--> 37 nnnnnnngag gagnnnnngg g                                            21
  40 <210> SEQ ID NO: 2
  41 <211> LENGTH: 21
  42 <212> TYPE: DNA
  43 <213> ORGANISM: Artificial Sequence
  45 <220> FEATURE:
  46 <223> OTHER INFORMATION: Artificail Sequence
  48 <220> FEATURE:
  49 <221> NAME/KEY: misc_feature
  50 <222> LOCATION: (4)..(8)
  51 <223> OTHER INFORMATION: n stands for any base
  54 <220> FEATURE:
  55 <221> NAME/KEY: misc_feature
  56 <222> LOCATION: (15)..(21)
  57 <223> OTHER INFORMATION: n stands for any base
  60 <400> SEQUENCE: 2
W--> 61 cccnnnnnct cctcnnnnnn n                                            21
  64 <210> SEQ ID NO: 3
```

Handwritten annotations:

pp 1-7

FYI: "Artificial" is misspelled. This is an insufficient explanation for <213> Artificial Sequence (give source of genetic material. See item 11 on Error Summary Sheet.)

Does Not Comply
Corrected Diskette Needed

same error

Please correct the above error in subsequent sequences

RAW SEQUENCE LISTING   DATE: 03/22/2005
PATENT APPLICATION: US/10/527,258   TIME: 09:49:38

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\03222005\J527258.raw

```
 65 <211> LENGTH: 23                    no Explanations in <2207-<223> section
 66 <212> TYPE: DNA
 67 <213> ORGANISM: Artificial           see p. 7 for error
 69 <220> FEATURE:                            Explanation
 70 <221> NAME/KEY: misc_feature
 71 <222> LOCATION: (2)..(10)
 72 <223> OTHER INFORMATION: n stands for any base.
 75 <220> FEATURE:
 76 <221> NAME/KEY: misc_feature
 77 <222> LOCATION: (17)..(23)
 78 <223> OTHER INFORMATION: n stands for any base.
 81 <400> SEQUENCE: 3
W--> 82 cnnnnnnnnn tccgccnnnn nnn                                    23
 85 <210> SEQ ID NO: 4
 86 <211> LENGTH: 24
 87 <212> TYPE: DNA               same error
 88 <213> ORGANISM: Artificial
 90 <220> FEATURE:
 91 <221> NAME/KEY: misc_feature
 92 <222> LOCATION: (1)..(7)
 93 <223> OTHER INFORMATION: n stands for any base.
 96 <220> FEATURE:
 97 <221> NAME/KEY: misc_feature
 98 <222> LOCATION: (14)..(22)
 99 <223> OTHER INFORMATION: n stands for any base.
102 <400> SEQUENCE: 4
W--> 103 nnnnnnnggc ggannnnnnn nngt                                  24
106 <210> SEQ ID NO: 5
107 <211> LENGTH: 23
108 <212> TYPE: DNA               same
109 <213> ORGANISM: Artificial
111 <220> FEATURE:
112 <221> NAME/KEY: misc_feature
113 <222> LOCATION: (1)..(7)
114 <223> OTHER INFORMATION: n stands for any base.
117 <220> FEATURE:
118 <221> NAME/KEY: misc_feature
119 <222> LOCATION: (14)..(18)
120 <223> OTHER INFORMATION: n stands for any base.
123 <400> SEQUENCE: 5
W--> 124 nnnnnnngag gagnnnnngg gac                                   23
127 <210> SEQ ID NO: 6
128 <211> LENGTH: 24
129 <212> TYPE: DNA
130 <213> ORGANISM: Artificial
132 <220> FEATURE:
133 <221> NAME/KEY: misc_feature
134 <222> LOCATION: (1)..(7)
135 <223> OTHER INFORMATION: n stands for any base.
```

```
     138 <220> FEATURE:
     139 <221> NAME/KEY: misc_feature
     140 <222> LOCATION: (14)..(22)
     141 <223> OTHER INFORMATION: n stands for any base.
     144 <400> SEQUENCE: 6
W--> 145 nnnnnnnggc ggannnnnnn nngt                                    24
     148 <210> SEQ ID NO: 7
     149 <211> LENGTH: 20
     150 <212> TYPE: DNA
     151 <213> ORGANISM: Artificial
     153 <220> FEATURE:
     154 <221> NAME/KEY: misc_feature
     155 <222> LOCATION: (1)..(7)
     156 <223> OTHER INFORMATION: n stands for any base.
     159 <220> FEATURE:
     160 <221> NAME/KEY: misc_feature
     161 <222> LOCATION: (14)..(14)
     162 <223> OTHER INFORMATION: n stands for any base.
     165 <400> SEQUENCE: 7
W--> 166 nnnnnnngag gagngtgcag                                         20
     169 <210> SEQ ID NO: 8
     170 <211> LENGTH: 22
     171 <212> TYPE: DNA
     172 <213> ORGANISM: Artificial
     174 <220> FEATURE:
     175 <221> NAME/KEY: misc_feature
     176 <222> LOCATION: (9)..(9)
     177 <223> OTHER INFORMATION: n stands for any base.
     180 <220> FEATURE:
     181 <221> NAME/KEY: misc_feature
     182 <222> LOCATION: (16)..(22)
     183 <223> OTHER INFORMATION: n stands for any base.
     186 <400> SEQUENCE: 8
W--> 187 tactgcacnc tcctcnnnnn nn                                       22
     190 <210> SEQ ID NO: 9
     191 <211> LENGTH: 23
     192 <212> TYPE: DNA
     193 <213> ORGANISM: Artificial
     195 <220> FEATURE:
     196 <221> NAME/KEY: misc_feature
     197 <222> LOCATION: (3)..(10)
     198 <223> OTHER INFORMATION: n stands for any base.
     201 <220> FEATURE:
     202 <221> NAME/KEY: misc_feature
     203 <222> LOCATION: (17)..(23)
     204 <223> OTHER INFORMATION: n stands for any base.
     207 <400> SEQUENCE: 9
W--> 208 acnnnnnnnn ctcctcnnnn nnn                                      23
     211 <210> SEQ ID NO: 10
```

```
212 <211> LENGTH: 25
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial
216 <220> FEATURE:
217 <221> NAME/KEY: misc_feature
218 <222> LOCATION: (1)..(7)
219 <223> OTHER INFORMATION: n stands for any base.
222 <220> FEATURE:
223 <221> NAME/KEY: misc_feature
224 <222> LOCATION: (14)..(21)
225 <223> OTHER INFORMATION: n stands for any base.
228 <220> FEATURE:
229 <221> NAME/KEY: misc_feature
230 <222> LOCATION: (24)..(25)
231 <223> OTHER INFORMATION: n stands for any base.
234 <400> SEQUENCE: 10
```

W--> 235 **nnnnnnngag gagnnnnnnn ngtnn**   25

```
238 <210> SEQ ID NO: 11
239 <211> LENGTH: 23
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial
243 <220> FEATURE:
244 <221> NAME/KEY: misc_feature
245 <222> LOCATION: (1)..(7)
246 <223> OTHER INFORMATION: n stands for any base.
249 <220> FEATURE:
250 <221> NAME/KEY: misc_feature
251 <222> LOCATION: (14)..(14)
252 <223> OTHER INFORMATION: n stands for any base.
255 <400> SEQUENCE: 11
```

W--> 256 **nnnnnnngag gagngtgcag tac**   23

```
259 <210> SEQ ID NO: 12
260 <211> LENGTH: 23
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial
264 <220> FEATURE:
265 <221> NAME/KEY: misc_feature
266 <222> LOCATION: (1)..(7)
267 <223> OTHER INFORMATION: n stands for any base.
270 <220> FEATURE:
271 <221> NAME/KEY: misc_feature
272 <222> LOCATION: (14)..(21)
273 <223> OTHER INFORMATION: n stands for any base.
276 <400> SEQUENCE: 12
```

W--> 277 **nnnnnnngag gagnnnnnnn ngt**   23

```
280 <210> SEQ ID NO: 13
281 <211> LENGTH: 20
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial
```

```
    285 <220> FEATURE:
    286 <221> NAME/KEY: misc_feature
    287 <222> LOCATION: (1)..(7)
    288 <223> OTHER INFORMATION: n stands for any base.
    291 <220> FEATURE:
    292 <221> NAME/KEY: misc_feature
    293 <222> LOCATION: (14)..(14)
    294 <223> OTHER INFORMATION: n stands for any base.
    297 <400> SEQUENCE: 13
W--> 298 nnnnnnngag gagngtgcag                                      20
    301 <210> SEQ ID NO: 14
    302 <211> LENGTH: 22
    303 <212> TYPE: DNA
    304 <213> ORGANISM: Artificial
    306 <220> FEATURE:
    307 <221> NAME/KEY: misc_feature
    308 <222> LOCATION: (9)..(9)
    309 <223> OTHER INFORMATION: n stands for any base.
    312 <220> FEATURE:
    313 <221> NAME/KEY: misc_feature
    314 <222> LOCATION: (16)..(22)
    315 <223> OTHER INFORMATION: n stands for any base.
    318 <400> SEQUENCE: 14
W--> 319 tactgcacnc tcctcnnnnn nn                                   22
    322 <210> SEQ ID NO: 15
    323 <211> LENGTH: 36
    324 <212> TYPE: DNA
    325 <213> ORGANISM: Artificial
    327 <220> FEATURE:
    328 <221> NAME/KEY: misc_feature
    329 <222> LOCATION: (1)..(7)
    330 <223> OTHER INFORMATION: n stands for any base.
    333 <220> FEATURE:
    334 <221> NAME/KEY: misc_feature
    335 <222> LOCATION: (14)..(14)
    336 <223> OTHER INFORMATION: n stands for any base.
    339 <220> FEATURE:
    340 <221> NAME/KEY: misc_feature
    341 <222> LOCATION: (24)..(36)
    342 <223> OTHER INFORMATION: n stands for any base.
    345 <400> SEQUENCE: 15
W--> 346 nnnnnnngag gagngtgcag tacnnnnnnn nnnnnn                    36
    349 <210> SEQ ID NO: 16
    350 <211> LENGTH: 34
    351 <212> TYPE: DNA
    352 <213> ORGANISM: Artificial
    354 <220> FEATURE:
    355 <221> NAME/KEY: misc_feature
    356 <222> LOCATION: (1)..(11)
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/22/2005
PATENT APPLICATION: US/10/527,258   TIME: 09:49:39

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\03222005\J527258.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1,2,3,4,5,6,7,14,15,16,17,18
Seq#:2; N Pos. 4,5,6,7,8,15,16,17,18,19,20,21
Seq#:3; N Pos. 2,3,4,5,6,7,8,9,10,17,18,19,20,21,22,23
Seq#:4; N Pos. 1,2,3,4,5,6,7,14,15,16,17,18,19,20,21,22
Seq#:5; N Pos. 1,2,3,4,5,6,7,14,15,16,17,18
Seq#:6; N Pos. 1,2,3,4,5,6,7,14,15,16,17,18,19,20,21,22
Seq#:7; N Pos. 1,2,3,4,5,6,7,14
Seq#:8; N Pos. 9,16,17,18,19,20,21,22
Seq#:9; N Pos. 3,4,5,6,7,8,9,10,17,18,19,20,21,22,23
Seq#:10; N Pos. 1,2,3,4,5,6,7,14,15,16,17,18,19,20,21,24,25
Seq#:11; N Pos. 1,2,3,4,5,6,7,14
Seq#:12; N Pos. 1,2,3,4,5,6,7,14,15,16,17,18,19,20,21
Seq#:13; N Pos. 1,2,3,4,5,6,7,14
Seq#:14; N Pos. 9,16,17,18,19,20,21,22
Seq#:15; N Pos. 1,2,3,4,5,6,7,14,24,25,26,27,28,29,30,31,32,33,34,35,36
Seq#:16; N Pos. 1,2,3,4,5,6,7,8,9,10,11,21,28,29,30,31,32,33,34
Seq#:17; N Pos. 1,2,3,4,5,6,7,14,15,16,17,18,19,20,21,22,25,26
Seq#:18; N Pos. 3,4,5,6,7,8,9,10,11,18,19,20,21,22,23,24
Seq#:19; N Pos. 1,2,3,4,5,6,7,14,24,25,26,27,28,29,30,31,32,33,34,35,36,39
Seq#:19; N Pos. 40,41,42,43,44,45,46,47,54,55,56,57,58,59,60
Seq#:20; N Pos. 1,2,3,4,5,6,7,14,15,16,17,18,19,20,21,22,25,26,27,28,29,30
Seq#:20; N Pos. 31,32,33,34,35,36,37,47,54,55,56,57,58,59,60
Seq#:21; N Pos. 1,2,3,4,5,6,7,14
Seq#:22; N Pos. 8,15,16,17,18,19,20,21
Seq#:23; N Pos. 1,2,3,4,5,6,7,14,15,16,17,18,19,20,21,22
Seq#:24; N Pos. 1,2,3,4,5,6,7,8,9,16,17,18,19,20,21,22
Seq#:25; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13
Seq#:26; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13
Seq#:30; N Pos. 21,22
Seq#:31; N Pos. 20,21,22,23,24,25,26,27,28,29,30,31,32
Seq#:34; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13
Seq#:35; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13
Seq#:36; N Pos. 3,4,5,6,7,8,9,10,11,12,13,14,15,18,19,20,21,22,23,24,25,26
Seq#:36; N Pos. 27,28,29,30,33,34,35,36,37,38,39,40,41,42,43,44,45,48,49,50
Seq#:36; N Pos. 51,52,53,54,55,56,57,58,59,60,63,64,65,66,67,68,69,70,71,72
Seq#:36; N Pos. 73,74,75,78,79,80,81,82,83,84,85,86,87,88,89,90
Seq#:37; N Pos. 3,4,5,6,7,8,9,10,11,12,13,14,15,18,19,20,21,22,23,24,25,26
Seq#:37; N Pos. 27,28,29,30,33,34,35,36,37,38,39,40,41,42,43,44,45,48,49,50
Seq#:37; N Pos. 51,52,53,54,55,56,57,58,59,60,63,64,65,66,67,68,69,70,71,72
Seq#:37; N Pos. 73,74,75,78,79,80,81,82,83,84,85,86,87,88,89,90
Seq#:65; N Pos. 20,21

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/22/2005
PATENT APPLICATION: US/10/527,258   TIME: 09:49:39

Input Set : **A:\PTO.SR.txt**
Output Set: **N:\CRF4\03222005\J527258.raw**

Seq#:3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,21,22,23,24,25,26,27,28,29,30,31
Seq#:32,33,34,35,36,37,59,60,61,62,63,64,65

Use of <220> Feature(NEW RULES): *error explanation*
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:27,28,29,32,33,59,60,61,62,63,64 *3,4,5,6,7,8,9,10,11,12,13,14,15,16,*
17,18,21,22,23,24,25,26,30,31,34,35,36,37,
65

VERIFICATION SUMMARY
DATE: 03/22/2005
PATENT APPLICATION: **US/10/527,258**
TIME: 09:49:39

Input Set : **A:\PTO.SR.txt**
Output Set: **N:\CRF4\03222005\J527258.raw**

```
L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:145 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:619 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:627 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial
L:627 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial
L:627 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:627
L:636 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:28, <213>
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L:636 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:28,Line#:636
L:645 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>
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L:645 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
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L:645 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:645
L:661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:684 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:32, <213>
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L:684 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:32, <213>
ORGANISM:Artificial
L:684 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:684
L:693 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:33, <213>
ORGANISM:Artificial
L:693 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:33, <213>
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ORGANISM:Artificial
L:693 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:33,Line#:693
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
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VERIFICATION SUMMARY　　　　　　　　　DATE: 03/22/2005
PATENT APPLICATION: **US/10/527,258**　　　TIME: 09:49:39

Input Set : **A:\PTO.SR.txt**
Output Set: **N:\CRF4\03222005\J527258.raw**

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M:341 Repeated in SeqNo=36
L:816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
M:341 Repeated in SeqNo=37
L:1015 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:59, <213>
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L:1015 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:59, <213>
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L:1015 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:59,Line#:1015
L:1024 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:60, <213>
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L:1024 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:60, <213>
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L:1024 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:60,Line#:1024
L:1033 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:61, <213>
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L:1042 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:62,Line#:1042
L:1051 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:63, <213>
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ORGANISM:Artificial
L:1051 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:63,Line#:1051
L:1060 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:64, <213>
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L:1060 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:64, <213>
ORGANISM:Artificial
L:1060 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:64,Line#:1060
L:1076 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:0
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